REMARKS

As amended, claims 28-58 (and new claims 59-60) now relate to a single general inventive concept under PCT Rule 13.1 because they are restricted to L1 **cytotoxic** T-cell epitopes, none of which are not known in the prior art. The de Gruijl (1999) reference, cited by the Office in support of the present restriction requirement, discloses only the T-**helper** cell epitopes P1 and P2; this reference does not cite any cytotoxic T-cell epitopes (see page 401, left col., paragraph 4). Therefore, the claims as currently amended belong to a single general inventive concept under PCT Rule 13.1, and neither a restriction or election requirement is justified. The requirement of electing a single amino acid sequence is also not in line with PCT Rule 13.1, and this requirement should also be withdrawn.

For the record, however, should the Office maintain the restriction and election requirements, Applicants elect for initial examination Group II (claims 28 and 32-38) and the amino acid sequence ICWGNQLFV. New dependent claims 59-60 also fall within Group II. For the reasons stated above, this election is made with traverse.

If there are any charges or any credits, please apply them to Deposit Account No. 03-2095.

Respectfully submitted,

Date: 9 July 2003

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

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|---|---|---|---|
| Applicant: | Ingrid Jochmus et al. | Art Unit: | 1648 |
| Serial No.: | 09/980,177 | Examiner: | A. R. Salimi |
| Filed: | May 2, 2002 | Customer No.: | 21559 |
| Title: | CYTOTOXIC T-CELL EPITOPES OF THE PAPILLOMA VIRUS L1-PROTEIN AND USE THEREOF IN DIAGNOSIS AND THERAPY | | |

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Version with Markings to Show Changes Made

In the claims:

Amend claims 28-30 and add claims 59 and 60 as follows.

28. (Currently Amended) A cytotoxic T-cell epitope having an amino acid sequence ILVPKVSGL (SEQ ID NO: 1), RLVWACVGV (SEQ ID NO: 2), HLFNRAGTV (SEQ ID NO: 3), YLRREQMFV (SEQ ID NO: 4), TLQANKSEV (SEQ ID NO: 5), ILEDWNFGL (SEQ ID NO: 6), SLWLPSEATVYL (SEQ ID NO: 7), NLASSNYFPT (SEQ ID NO: 8), TLTADVMTYI (SEQ ID NO: 9), YLPPVPVSKV (SEQ ID NO: 10), YDLQFIFQL (SEQ ID NO: 11), ICWGNQLFV (SEQ ID NO: 12), FYNPDTQRL (SEQ ID NO: 13), [MHGDTPTLH (SEQ ID

NO: 14), ETTDLYCY (SEQ ID NO: 15), QAEPDRAHYN (SEQ ID NO: 16), SMVTSDAQI (SEQ ID NO: 17),] and/or a functionally active variant thereof.

29. (Currently Amended) The cytotoxic T-cell epitope as claimed in claim 28, wherein said variant has a sequence homology to ILVPKVSGL (SEQ ID NO: 1), RLVWACVGV (SEQ ID NO: 2), HLFNRAGTV (SEQ ID NO: 3), YLRREQMFV (SEQ ID NO: 4), TLQANKSEV (SEQ ID NO: 5), ILEDWNFGL (SEQ ID NO: 6), SLWLPSEATVYL (SEQ ID NO: 7), NLASSNYFPT (SEQ ID NO: 8), TLTADVMTYI (SEQ ID NO: 9), YLPPVPVSKV (SEQ ID NO: 10), YDLQFIFQL (SEQ ID NO: 11), ICWGNQLFV (SEQ ID NO: 12), FYNPDTQRL (SEQ ID NO: 13), [MHGDTPTLH (SEQ ID NO: 14), ETTDLYCY (SEQ ID NO: 15), QAEPDRAHYN (SEQ ID NO: 16), SMVTSDAQI (SEQ ID NO: 17),] of at least approx. 65%, preferably at least approx. 75% and in particular at least approx. 85% at the amino acid level.

30. (Currently Amended) The cytotoxic T-cell epitope as claimed in claim 28, wherein said variant is structurally homologous to ILVPKVSGL (SEQ ID NO: 1), RLVWACVGV (SEQ ID NO: 2), HLFNRAGTV (SEQ ID NO: 3), YLRREQMFV (SEQ ID NO: 4), TLQANKSEV (SEQ ID NO: 5), ILEDWNFGL (SEQ ID NO: 6), SLWLPSEATVYL (SEQ ID NO: 7), NLASSNYFPT (SEQ ID NO: 8), TLTADVMTYI (SEQ ID NO: 9), YLPPVPVSKV (SEQ ID NO: 10), YDLQFIFQL (SEQ ID NO: 11), ICWGNQLFV (SEQ ID NO: 12), or FYNPDTQRL (SEQ ID NO: 13)[, MHGDTPTLH (SEQ ID NO: 14), ETTDLYCY (SEQ ID NO: 15), QAEPDRAHYN (SEQ ID NO: 16), or SMVTSDAQI (SEQ ID NO: 17)].

59. (New) The compound as claimed in claim 32, wherein said variant has a sequence homology to ILVPKVSGL (SEQ ID NO: 1), RLVWACVGV (SEQ ID NO: 2), HLFNRAGTV (SEQ ID NO: 3), YLRREQMFV (SEQ ID NO: 4), TLQANKSEV (SEQ ID NO: 5), ILEDWNFGL (SEQ ID NO: 6), SLWLPSEATVYL (SEQ ID NO: 7), NLASSNYFPT (SEQ ID NO: 8), TLTADVMTYI (SEQ ID NO: 9), YLPPVPVSKV (SEQ ID NO: 10), YDLQFIFQL (SEQ ID NO: 11), ICWGNQLFV (SEQ ID NO: 12), FYNPDTQRL (SEQ ID NO: 13), of at least approx. 65%, preferably at least approx. 75% and in particular at least approx. 85% at the amino acid level.

60. (New) The compound as claimed in claim 32, wherein said variant is structurally homologous to ILVPKVSGL (SEQ ID NO: 1), RLVWACVGV (SEQ ID NO: 2), HLFNRAGTV(SEQ ID NO: 3), YLRREQMFV (SEQ ID NO: 4), TLQANKSEV (SEQ ID NO: 5), ILEDWNFGL (SEQ ID NO: 6), SLWLPSEATVYL (SEQ ID NO: 7), NLASSNYFPT (SEQ ID NO: 8), TLTADVMTYI (SEQ ID NO: 9), YLPPVPVSKV (SEQ ID NO: 10), YDLQFIFQL (SEQ ID NO: 11), ICWGNQLFV (SEQ ID NO: 12), or FYNPDTQRL (SEQ ID NO: 13).